

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/322,021

DATE: 07/30/1999
 TIME: 14:41:24

INPUT SET: S32704.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
 2
 3 (1) General Information:
 4
 5 (i) APPLICANT: ARMITAGE, RICHARD
 6 FANSLow, WILLIAM
 7 SPRIGGS, MELANIE
 8 SRINIVASAN, SUBHASHINI
 9 GIBSON, MARYLOU
 10
 11 (ii) TITLE OF INVENTION: NOVEL CYTOKINE
 12
 13 (iii) NUMBER OF SEQUENCES: 23
 14
 15 (iv) CORRESPONDENCE ADDRESS:
 16 (A) ADDRESSEE: IMMUNEX CORPORATION
 17 (B) STREET: 51 UNIVERSITY STREET
 18 (C) CITY: SEATTLE
 19 (D) STATE: WASHINGTON
 20 (E) COUNTRY: USA
 21 (F) ZIP: 98101
 22
 23 (v) COMPUTER READABLE FORM:
 24 (A) MEDIUM TYPE: Floppy disk
 25 (B) COMPUTER: Apple Macintosh
 26 (C) OPERATING SYSTEM: Apple Operating System 7.1
 27 (D) SOFTWARE: Microsoft Word for Apple, version 5.1a
 28
 29 (vi) CURRENT APPLICATION DATA:
 30 (A) APPLICATION NUMBER: 09/322,021
 31 (B) FILING DATE:
 32 (C) CLASSIFICATION:
 33
 34 (vii) PRIOR APPLICATION DATA:
 35 (A) APPLICATION NUMBER: 08/249,189
 36 (B) FILING DATE:
 37 (C) CLASSIFICATION:
 38
 39 (vii) PRIOR APPLICATION DATA:
 40 (A) APPLICATION NUMBER: 07/805,723
 41 (B) FILING DATE: December 5, 1991
 42 (C) CLASSIFICATION: 514
 43
 44 (vii) PRIOR APPLICATION DATA:
 45 (A) APPLICATION NUMBER: 07/783,707
 46 (B) FILING DATE: October 25, 1991

ENTERED

-->dc

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--> 47 (C) CLASSIFICATION: 514
48
49 (viii) ATTORNEY/AGENT INFORMATION:
50 (A) NAME: Perkins, Patricia A.
51 (B) REGISTRATION NUMBER: 34,693
52 (C) REFERENCE/DOCKET NUMBER: 2802-C
53
54 (ix) TELECOMMUNICATION INFORMATION:
55 (A) TELEPHONE: 2065870430
56 (B) TELEFAX: 2065870606
57
58
59 (2) INFORMATION FOR SEQ ID NO:1:
60
61 (i) SEQUENCE CHARACTERISTICS:
62 (A) LENGTH: 783 base pairs
63 (B) TYPE: nucleic acid
64 (C) STRANDEDNESS: single
65 (D) TOPOLOGY: linear
66
67 (ii) MOLECULE TYPE: cDNA
68
69 (iii) HYPOTHETICAL: NO
70
71 (iv) ANTI-SENSE: NO
72
73 (vi) ORIGINAL SOURCE:
74 (A) ORGANISM: MOUSE
75
76 (vii) IMMEDIATE SOURCE:
77 (B) CLONE: CD40-L
78
79 (ix) FEATURE:
80 (A) NAME/KEY: CDS
81 (B) LOCATION: 1..783
82
83
84 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
85
86 ATG ATA GAA ACA TAC AGC CAA CCT TCC CCC AGA TCC GTG GCA ACT GGA 48
87 Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly
88 1 5 10 15
89
90 CTT CCA GCG AGC ATG AAG ATT TTT ATG TAT TTA CTT ACT GTT TTC CTT 96
91 Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
92 20 25 30
93
94 ATC ACC CAA ATG ATT GGA TCT GTG CTT TTT GCT GTG TAT CTT CAT AGA 144
95 Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg
96 35 40 45
97
98 AGA TTG GAT AAG GTC GAA GAG GAA GTA AAC CTT CAT GAA GAT TTT GTA 192
99 Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val

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100	50	55	60	
101				
102	TTC ATA AAA AAG CTA AAG AGA TGC AAC AAA GGA GAA GGA TCT TTA TCC			240
103	Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser			
104	65	70	75	80
105				
106	TTG CTG AAC TGT GAG GAG ATG AGA AGG CAA TTT GAA GAC CTT GTC AAG			288
107	Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys			
108		85	90	95
109				
110	GAT ATA ACG TTA AAC AAA GAA GAG AAA AAA GAA AAC AGC TTT GAA ATG			336
111	Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met			
112		100	105	110
113				
114	CAA AGA GGT GAT GAG GAT CCT CAA ATT GCA GCA CAC GTT GTA AGC GAA			384
115	Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu			
116		115	120	125
117				
118	GCC AAC AGT AAT GCA GCA TCC GTT CTA CAG TGG GCC AAG AAA GGA TAT			432
119	Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr			
120		130	135	140
121				
122	TAT ACC ATG AAA AGC AAC TTG GTA ATG CTT GAA AAT GGG AAA CAG CTG			480
123	Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu			
124	145	150	155	160
125				
126	ACG GTT AAA AGA GAA GGA CTC TAT TAT GTC TAC ACT CAA GTC ACC TTC			528
127	Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe			
128		165	170	175
129				
130	TGC TCT AAT CGG GAG CCT TCG AGT CAA CGC CCA TTC ATC GTC GGC CTC			576
131	Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu			
132		180	185	190
133				
134	TGG CTG AAG CCC AGC AGT GGA TCT GAG AGA ATC TTA CTC AAG GCG GCA			624
135	Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala			
136		195	200	205
137				
138	AAT ACC CAC AGT TCC TCC CAG CTT TGC GAG CAG CAG TCT GTT CAC TTG			672
139	Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu			
140		210	215	220
141				
142	GGC GGA GTG TTT GAA TTA CAA GCT GGT GCT TCT GTG TTT GTC AAC GTG			720
143	Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val			
144	225	230	235	240
145				
146	ACT GAA GCA AGC CAA GTG ATC CAC AGA GTT GGC TTC TCA TCT TTT GGC			768
147	Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly			
148		245	250	255
149				
150	TTA CTC AAA CTC TGA			783
151	Leu Leu Lys Leu			
152		260		

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153

154

155 (2) INFORMATION FOR SEQ ID NO:2:

156

157 (i) SEQUENCE CHARACTERISTICS:

158 (A) LENGTH: 260 amino acids

159 (B) TYPE: amino acid

160 (D) TOPOLOGY: linear

161

162 (ii) MOLECULE TYPE: protein

163

164 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

165

166 Met Ile Glu Thr Tyr Ser Gln Pro Ser Pro Arg Ser Val Ala Thr Gly
167 1 5 10 15

168

169 Leu Pro Ala Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu
170 20 25 30

171

172 Ile Thr Gln Met Ile Gly Ser Val Leu Phe Ala Val Tyr Leu His Arg
173 35 40 45

174

175 Arg Leu Asp Lys Val Glu Glu Glu Val Asn Leu His Glu Asp Phe Val
176 50 55 60

177

178 Phe Ile Lys Lys Leu Lys Arg Cys Asn Lys Gly Glu Gly Ser Leu Ser
179 65 70 75 80

180

181 Leu Leu Asn Cys Glu Glu Met Arg Arg Gln Phe Glu Asp Leu Val Lys
182 85 90 95

183

184 Asp Ile Thr Leu Asn Lys Glu Glu Lys Lys Glu Asn Ser Phe Glu Met
185 100 105 110

186

187 Gln Arg Gly Asp Glu Asp Pro Gln Ile Ala Ala His Val Val Ser Glu
188 115 120 125

189

190 Ala Asn Ser Asn Ala Ala Ser Val Leu Gln Trp Ala Lys Lys Gly Tyr
191 130 135 140

192

193 Tyr Thr Met Lys Ser Asn Leu Val Met Leu Glu Asn Gly Lys Gln Leu
194 145 150 155 160

195

196 Thr Val Lys Arg Glu Gly Leu Tyr Tyr Val Tyr Thr Gln Val Thr Phe
197 165 170 175

198

199 Cys Ser Asn Arg Glu Pro Ser Ser Gln Arg Pro Phe Ile Val Gly Leu
200 180 185 190

201

202 Trp Leu Lys Pro Ser Ser Gly Ser Glu Arg Ile Leu Leu Lys Ala Ala
203 195 200 205

204

205 Asn Thr His Ser Ser Ser Gln Leu Cys Glu Gln Gln Ser Val His Leu

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206          210          215          220
207
208 Gly Gly Val Phe Glu Leu Gln Ala Gly Ala Ser Val Phe Val Asn Val
209 225          230          235          240
210
211 Thr Glu Ala Ser Gln Val Ile His Arg Val Gly Phe Ser Ser Phe Gly
212          245          250          255
213
214 Leu Leu Lys Leu
215          260
216
217

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(2) INFORMATION FOR SEQ ID NO:3:

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220 (i) SEQUENCE CHARACTERISTICS:
221 (A) LENGTH: 740 base pairs
222 (B) TYPE: nucleic acid
223 (C) STRANDEDNESS: single
224 (D) TOPOLOGY: linear

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225
226 (ii) MOLECULE TYPE: cDNA

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227
228 (iii) HYPOTHETICAL: NO

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229
230 (iv) ANTI-SENSE: NO

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231
232 (vi) ORIGINAL SOURCE:
233 (A) ORGANISM: HUMAN

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234
235 (vii) IMMEDIATE SOURCE:
236 (B) CLONE: IgG1 Fc

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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240
241 CGGTACCGCT AGCGTCGACA GGCCTAGGAT ATCGATACGT AGAGCCCAGA TCTTGTGACA      60
242
243 AAACCTCACAC ATGCCACCG TGCCAGCAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC      120
244
245 TCTTCCCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG GTCACATGCG      180
246
247 TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC GTGGACGGCG      240
248
249 TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC ACGTACCGGG      300
250
251 TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAC TACAAGTGCA      360
252
253 AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TGCAGAAAAC CATCTCCAAA GCCAAAGGGC      420
254
255 AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGATGAGCTG ACCAAGAACC      480
256
257 AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG GCACATCGCC GTGGAGTGGG      540
258

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PAGE: 1

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/09/322,021

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Line	Error	Original Text
42	Wrong Classification	(C) CLASSIFICATION:514
47	Wrong Classification	(C) CLASSIFICATION:514